then transposing the resulting frequencies into the audible domain, thus providing a code which allows the stimulation of the biosynthesis of said protein, the code relative to its inhibition being obtained through a symmetrization of the logarithms of the frequencies just obtained relatively to their central value taken as origin;

(b) determining the musical periods by spotting similar sequences of notes and signatures;

(c) determining the lengths of the notes by rectifying first collectively then individually the periods as determined in step (b) through an adjustment of phrasing to measure, controlled using a keyboard featuring a 'one key play' device;

(d) determining the tone quality through the retroaction of the whole set of amino acids of the protein on the harmonic structure of each; and

B. playing said sequence of musical notes *in situ* to stimulate or inhibit said protein biosynthesis, either directly, or indirectly by using a recording on any proper support of the sequence of musical notes heretofore obtained.

14. (New) The method according to Claim 13, characterized by producing, using a properly adjusted instrument, a sequence of musical notes, said notes being associated to amino acids according to the following code, specific to the epigenetic stimulation of protein biosynthesis, according to the chromatic tempered scale in ascending order:

Gly = low A; Ala = C; Ser = E; Pro, Val, Thr, Cys = F; Leu, Ile, Asn, Asp = G; Gln, Lys, Glu, Met = A; His = B flat; Phe, SeC = B; Arg, Tyr = sharp C; Trp = sharp D.

15. (New) The method according to Claim 13, characterized in producing, using a properly adjusted instrument, a sequence of musical notes, said notes being associated to amino acids according to the following codes, specific to the epigenetic inhibition of protein biosynthesis and derived from the following code, specific to the epigenetic stimulation of protein biosynthesis, according to the chromatic tempered scale in ascending order:

Gly = low A; Ala = C; Ser = E; Pro, Val, Thr, Cys = F; Leu, Ile, Asn, Asp = G; Gln, Lys, Glu, Met = A; His = B flat; Phe, SeC = B; Arg, Tyr = sharp C; Trp = sharp D

by symmetrization of the notes relatively to the central G within the chromatic tempered scale, to yield in ascending order:

Trp = C; Arg, Tyr = D; Phe, SeC = E flat; His = E; Gln, Lys, Glu, Met = F; Leu, Ile, Asn, Asp = G; Pro, Val, Thr, Cys = A; Ser = B flat; Ala = sharp D; Gly = sharp F.

16. (New) The method according to Claim 13 or Claim 14, characterized in further stabilizing said protein synthesis using a proper colored light transposition obtained by transposing the quantum vibrations associated to the mature protein once spatially fold over itself, according to a code which is derived from that obtained at the end of step (a) of Claim 14 specific to the stimulation of its biosynthesis, through the formula

$$\upsilon = \upsilon_{\circ_{\circ}} (\cosh)^{-1} (e^{(f/f_{\circ})\, Log \cosh i})$$

where f, $f_{\circ}$ are the musical frequencies and υ, $\upsilon_{\circ}$ the colored ones, with the indices $^{\circ}$ denoting the central values.

17. (New) A method according to Claim 16, characterized in that the spatial positions of the colors are those occupied by the amino acids in a three-dimensional spatial representation of said protein, the code being

Gly = dark red; Ala = bright red; Ser = orange; Pro, Val Thr, Cys = ochre; Leu, Ile, Asn, Asp = lemon yellow; Gln, Glu, Lys, Met = green; His = emerald; Phe = blue; Arg, Tyr = indigo; Trp = purple.

18. (New) The method according too Claim 13, wherein said protein is selected by systematically spotting the melodic similarities and counter-similarities from the protein sequences that are known and available in data banks so as to determine their metabolic